REMARKS

Claims 1-43 are pending in the application. By virtue of this submission, claims 1-43 have been canceled and replaced with claims 44-66. Support for amendments to the specification and claims can be found throughout the specification and the claims as originally filed. No new matter has been added.

In particular, support for the Brief Description of the Drawings can be found in the Examples section.

Support for the description of Figure 1 can be found, for example, at page 22, line 10.

Support for the description of Figure 2 can be found, for example, at page 22, lines 12-13.

Support for the description of Figure 3 can be found, for example, at page 22, lines 18-23.

Support for the description of Figure 4 can be found, for example, in Figure 4.

Support for the description of Figure 5 can be found, for example, at page 34, lines 11-13.

Support for the description of Figure 6 can be found, for example, at page 35, lines 19-20.

Support for the amendments to claims can be found as follows:

Claim	Support
44	Claim 1 presented in the Article 34 Amendment and Page 5, line 15 to page 6, line 2
45	Claim 3 presented in the Article 34 Amendment and Page 4, line 28 to page 5, line 5
46-48	Claim 4 presented in the Article 34 Amendment and Page 4, line 28 to page 5, line 5
49	Claim 2 presented in the Article 34 Amendment, Page 4, line 28 to page 5, line 5 and Figures 3 & 4
50-51	Claim 5 presented in the Article 34 Amendment
52-56	Claims 6-10 presented in the Article 34 Amendment, respectively
57	Claims 17-19 presented in the Article 34 Amendment and Page 9, line 16
58	Page 28, lines 4-5, Page 29, lines 10-11 and Page 32, lines 8-10
59	Claim 20 presented in the Article 34 Amendment
60	Claim 21 presented in the Article 34 Amendment, Page 6, lines 20-27 and Page 7, line 25 to page 8, line 1
61-62	Page 9, lines 1-5
63	Claims 21-22 presented in the Article 34 Amendment and Page 10, line 7 to page 11, line 1
64	Claims 21-22 presented in the Article 34 Amendment, Page 28, lines 4-5, Page 29, lines 10-11 and Page 32, lines 8-10
65	Claims 21-22 presented in the Article 34 Amendment and Page 10, line 7 to page 11, line 1
66	Claim 19 presented in the Article 34 Amendment and Page 12, line 28 to page 13, line 12

Cancellation and/or amendment of claims should in no way be construed as an acquiescence to any of the Examiner's rejections. The cancellation and/or amendments to the claims are being made solely to expedite prosecution of one set of claims to subject matter of potential clinical and/or commercial significance. Applicants reserve the option to further prosecute additional claims, including without limitation claims of the same or similar scope as the claims formerly pending in the instant patent application.

Following the claim amendments, most issues raised by the Examiner in the Office Action no longer apply; however, each issue is addressed below.

Improper Amendment

The Action noted that previously filed claim Amendments were based on the originally filed PCT application instead of the claims presented in the Article 34 amendment. As a result, the claim numbering was improper under 37 CFR §1.126 and correction was requested. After a brief discussion with the Examiner, Applicant's have decided to cancel all pending claims and replace them with a new set of claims starting at the next highest unused number in an effort to expedite prosecution of the application. Therefore, Applicant's submit that the current submission rectifies the errors in the previously filed amendments.

Specification

Abstract

The specification was objected to for not containing the Abstract on a separate sheet. Applicant's submit that since this is a 371 application, the cover sheet of the PCT application, which contains an Abstract, meets the requirements for an Abstract on a separate sheet under 37 CFR §1.72(b). However, in an effort to expedite prosecution, the Abstract from the cover of the International Publication WO 97/40167 presented on a separate sheet is being submitted along with this submission. Therefore, withdrawal of the objection is respectfully requested.

Arrangement

The specification was objected to for not being arranged into sections. Applicant's wish to point out that the arrangement indicated in 37 CFR §1.77 is simply a preferred arrangement and an Application need only include reference to applicable sections. By virtue of this submission, Applicant's have inserted the appropriate sections by amendment where applicable for this Application. Therefore, withdrawal of the objection is respectfully requested.

Sequence Listing

The specification was objected to for not referring to the nucleotide and amino acid sequences with a SEQ ID NO and also for containing sequences which were not part of the sequence listing. By virtue of this submission, the specification has been amended so that each reference to a nucleotide or amino acid sequence is followed by reference to the appropriate SEQ ID NO.

Additionally, Applicant's submit concurrently herewith a substitute sequence listing containing all of the sequences disclosed in the specification. The substitute sequence listing is believed to meet all of the requirements of 37 CFR §1.821-1.825. Therefore, reconsideration and withdrawal of the objection to the specification regarding the sequence listing is respectfully requested.

Applicant's wish to note that the primer sequences disclosed on page 28 were presented in the originally submitted sequence listing as SEQ ID NOs: 7 and 8. The primers on pages 29 and 32 are presented in the substitute listing as SEQ ID NOs: 11 and 12 and SEQ ID NOs: 13 and 14, respectively.

Figure 4 presents a list of modifications to specific nucleotide or amino acid residues presented in Figure 3. Specifically, the top portion of Figure 4 refers to bases 5260 to 8210 of the nucleotide sequence of Figure 3 further including the 14 specified modifications. This sequence was presented in the original sequence listing as SEQ ID NO: 9, but was inadvertantly missing nucleotides 5260-5619 of Figure 3 and the changes corresponding to this region listed in Figure 4. By virtue of this submission, SEQ ID NO: 9 has been corrected to include bases 5260 to 8210 of Figure 3 including the 14 changes listed in Figure 4. The nucleotide sequence specified in the top portion of Figure 4 encodes for a modified version of the ENV polypeptide which contains the 18 specified changes listed in the bottom portion of the figure. The ENV polypeptide is encoded by nucleotides 5620-7590 of Figure 3 and is presented in the sequence listing as SEQ ID NO: 6. The modified ENV polypeptide containing the 18 changes listed in the bottom portion of Figure 4 (i.e., a modified version of SEQ ID NO: 6 containing the specified changes) was presented in the original sequence listing as SEQ ID NO: 10.

The short amino acid sequences disclosed on page 23, lines 14 and 16 are presented in the substitute sequence listing as SEQ ID NOs: 15 and 16, respectively.

The sequence disclosed in Figure 6 is presented in the substitute sequence listing as SEQ ID NO: 17.

Figure 5

As suggested by the Examiner, reference to "Figure J" at page 34, line 13, has been amended to "Figure 5."

New Matter

The amendment filed July 19, 2000 was objected to for introducing new matter. In particular, the Action states that the sequences disclosed in SEQ ID NOs: 9 and 10 were not disclosed in the specification. As discussed above, the sequences presented in SEQ ID NOs: 9 and 10 were presented in Figure 4 and thus do not constitute new matter. Therefore, reconsideration and withdrawal of the objection is respectfully requested.

Claim Objections

The claim amendments made herein are believed to obviate the Examiner's objections. In particular, the claims have been amended to remove recitation of non-elected subjected matter and to no longer contain improper multiple dependent claims. Therefore, reconsideration and withdrawal of the objections is respectfully requested.

Double Patenting

The claim amendments made herein are believed to obviate the Examiner's objections. In particular, the claims have been amended so that no two claims contain the identical subject matter. Therefore, reconsideration and withdrawal of the objections is respectfully requested.

Claims 1-5, 17 and 19-22 Rejected under 35 U.S.C. §112, first paragraph

Written Description

Claims 1-5, 17 and 19-22 were rejected under 35 U.S.C. §112, first paragraph, for reasons of written description. The Action states that the specification does not provide any description for the terms "derivative," "expression product displaying a physiological or immunological activity" and "all non PoEV sequences." The Action further states that:

> The limited information is not deemed sufficient to reasonably convey to one skilled in the art that Applicant is in possession of polynucleotides besides SEQ ID No 1, 2, and 3 wherein SEQ ID NO 3 encodes the amino acid sequences disclosed in SEQ ID No 4, 5, and 6, at the time the application was filed. Thus it is concluded that the written description requirement is no satisfied for the claimed genus.

The rejection is respectfully traversed.

Applicants' respectfully disagree with the rejection, however, in an effort to expedite prosecution of the Application, claims 1-43 have been canceled and rewritten as claims 44-65. The claim amendments are believed to obviate the Examiner's rejection. In particular, the phrases "derivative," "expression product displaying a physiological or immunological activity" and "all non PoEV sequences" have been removed from the claims. .

The Action alleges that the specification is not sufficient to reasonably convey to one skilled in the art that the Applicants were in possession of the claimed genera at the time the application was filed. As amended, the genera is directed to an isolated polynucleotide fragment comprising (a) a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9; (b) a portion of a nucleotide sequence set forth in (a) which encodes for at least one porcine retrovirus polypeptide; (c) a nucleotide sequence which has at least 75% identity to a sequence set forth in (a) or (b); or (d) a nucleotide sequence which is complementary to a nucleotide sequence set forth in (a), (b) or (c).

The specification discloses the nucleotide sequence for SEQ ID NOs: 1, 2, 3 and 9 (see Figures 1-4). The specification further discloses portions of SEQ ID NOs: 1, 2, 3 and 9 which encode for at least one porcine retrovirus (see Figures 3 and 4). The Specification also discloses that nucleotide sequences having at least 75% identity to SEQ ID NOs: 1, 2, 3 and 9 may be

isolated by their ability to hybridize with these sequences (see e.g., pages 7-8). Therefore, the specification clearly supports that Applicants' were in possession of the claimed invention at the time of filing the Application. Accordingly, reconsideration and withdrawal of the rejection are respectfully requested.

Enablement

Claims 1-5 were rejected under 35 U.S.C. §112, first paragraph, for reasons of enablement. In particular, the action states that:

> ***[T]he specification, while being enabling for an isolated polynucleotide disclosed in SEQ ID NO: 1, 2 and 3 wherein the polynucleotides of SEQ ID NO: 2 and 3 have three open reading frames of 524, 1194 and 656 amino acids each, does not reasonably provide enablement ofr any other claimed embodiments. The specification does not enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the invention commensurate in scope with these claims.

The Rejection is respectfully traversed.

Applicants' respectfully disagree with the rejection, however, in an effort to expedite prosecution of the Application, claims 1-43 have been canceled and replaced with new claims 44-66. The claim amendments are believed to obviate the Examiner's rejections.

As discussed above, the amended claims are directed to an isolated polynucleotide fragment comprising (a) a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9; (b) a portion of a nucleotide sequence set forth in (a) which encodes for at least one porcine retrovirus polypeptide; (c) a nucleotide sequence which has at least 75% identity to a sequence set forth in (a) or (b); or (d) a nucleotide sequence which is complementary to a nucleotide sequence set forth in (a), (b) or (c).

The specification discloses and therefore clearly enables: (i) the nucleotide sequence for SEQ ID NOs: 1, 2, 3 and 9 (see Figures 1-4) and (ii) portions of SEQ ID NOs: 1, 2, 3 and 9 which encode for at least one porcine retrovirus (see Figures 3 and 4). The Specification also teaches that nucleotide sequences having at least 75% identity to SEQ ID NOs: 1, 2, 3 and 9 may be isolated by their ability to hybridize with these sequences (see e.g., pages 7-8). Therefore, the

specification clearly enables the claimed invention. Accordingly, reconsideration and withdrawal of the rejection are respectfully requested.

Claims 17 and 19-22 were rejected under 35 U.S.C. §112, first paragraph, for reasons of enablement. In particular, the action states that:

> The specification is not enabling for the invention of claims 17 and 19-22 because the specification does not provide sufficient guidance, evidence of working examples as to how an artisan would have made and used the claimed invention without undue experimentation.

The Rejection is respectfully traversed.

Applicants' respectfully disagree with the rejection, however, in an effort to expedite prosecution of the Application, claims 1-43 have been canceled and rewritten as new claims 44-66. The claim amendments are believed to obviate the Examiner's rejection. In particular, the claims directed to probes and primers, as amended, are directed to (i) oligonucleotides comprising at least 30 nucleotides which are fully complementary to a sequence set forth in SEQ ID NOs: 1, 2, 3 or 9 or (ii) a pair of oligonucleotide primers for use in PCR amplification wherein each primer comprises at least 10 nucleotides complementary to a sequence set forth in SEQ ID NO: 1, 2, 3 or 9, or a sequence complementary to a sequence set forth in SEQ ID NO: 1, 2, 3 or 9.

Use of oligonucleotide for detection of PoEV is clearly described in the specification (see e.g., pages 7-8). Furthermore, use of pairs of oligonucleotide primers for PCR amplification of PoEV is described in the specification (see e.g., pages 10-11 and the Examples). Furthermore, the Examples section provides the sequences for specific PoEV primers which were used for amplification of PoEV sequences (see e.g., pages 28-33). Therefore, the specification clearly enables the oligonucleotide primers and probes as claimed in the Application. Accordingly, reconsideration and withdrawal of the rejection is respectfully requested.

Claim 22 Rejected under 35 U.S.C. §112, second paragraph

Claim 22 was rejected under 35 U.S.C. §112, second paragraph, for being indefinite. In particular, the Action states that the claim sets forth the use of primers and polynucleotides without setting forth any steps involved in the method/process of use. The rejection is respectfully traversed.

Claims 1-43 have been canceled and rewritten as new claims 44-66. In particular, the use claims have been rewritten as method claims which set forth the specific steps for carrying out the method. The claim Amendments are believed to obviate the Examiner's rejection. Therefore, reconsideration and withdrawal of the rejection is respectfully requested.

Claims 1-5 Rejected under 35 U.S.C. §112, second paragraph

Claims 1-5 were rejected under 35 U.S.C. §112, second paragraph, for being indefinite.

In particular, claims 1 and 5 were rejected for recitation of the term "a physiological activity," claim 2 was rejected for recitation of the term "substantially similar" and claims 1-5 were rejected for recitation of the term "derivative." Claims 1-43 have been canceled and rewritten as new claims 44-66. The claim amendments are believed to obviate the rejection as the terms at issue have been removed from the claims. Therefore, reconsideration and withdrawal of the rejection are respectfully requested.

Claims 1-5 were rejected for recitation of the term "isolated polynucleotide fragment as shown in Figures 1, 2, 3, or 4" in the preamble. Claims 1-43 have been canceled and rewritten as new claims 44-66. The claim amendments are believed to obviate the rejection as the terms at issue have been removed from the preamble of the claims. Therefore, reconsideration and withdrawal of the rejection are respectfully requested.

Claims 1-5 were rejected for being indefinite because the Action states that it was unclear how the preamble related to parts (a)-(c) of the claims. Claims 1-43 have been canceled and rewritten as new claims 44-66. The claim amendments are believed to obviate the rejection. Therefore, reconsideration and withdrawal of the rejection are respectfully requested.

Claims 1-4 were rejected for recitation of the term "corresponding RNA sequence." Claims 1-43 have been canceled and rewritten as new claims 44-66. The claim amendments are

believed to obviate the rejection as the term at issue has been removed from the claims. Therefore, reconsideration and withdrawal of the rejection are respectfully requested.

Claims 1-5 parts (b)-(c) Rejected under 35 U.S.C. §102(e)

Claims 1-5 parts (b)-(c) were rejected under 35 U.S.C. §102(e) as being anticipated by Eiden et al. US Patent No. 6,033,905. The action states that:

> Eiden et al. teach retroviral vectors based on Gibbon Ape Leukemia virus. The sequence disclosed by Eiden et al sequence high similarities with the sequences disclosed in SEQ ID NO 1, 2, 3, 4, 5 etc. in regions of over 20 nucleotides or 16 amino acids (see sequence comparison results) and primers specific to these regions will hybridize to the sequence of SEQ ID NO: 1, 2, and 3.
>
> Since Gibbon Ape leukeimia virus encodes Gag, Pol, and ENV polynucleotides which have similar functions in all the lentiviruses, the invention of claims 1-5, parts (b)-(c) is anticipated by Eiden et al.

The rejection is respectfully traversed.

While Applicant's respectfully disagree with the rejection, claims 1-43 have been canceled and rewritten as claims 44-66 in an effort to expedite prosecution of the Application. The claim amendments are believed to have obviated the Examiner's rejections.

As amended the claims are directed to an isolated polynucleotide fragment comprising (a) a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9; (b) a portion of a nucleotide sequence set forth in (a) which encodes for at least one porcine retrovirus polypeptide; (c) a nucleotide sequence which has at least 75% identity to a sequence set forth in (a) or (b); or (d) a nucleotide sequence which is complementary to a nucleotide sequence set forth in (a), (b) or (c).

In contrast to claim 44 part (a), Eiden et al. does not teach a polynucleotide sequence comprising the sequence of SEQ ID NO: 1, 2, 3 or 9. Comparison of the genome of Gibbon Ape Leukemia Virus (GALV) with SEQ ID NO: 3 disclosed in the instant Application shows only 64% identity (see Attachment A).

In contrast to claim 44 part (b), Eiden et al. does not teach a portion of a SEQ ID NOs: 1, 2, 3 or 9 which encode for at least one porcine retrovirus polypeptide. Nucleotides 588-2162 of SEQ ID NO: 3 of the instant Application encode for a GAG polypeptide, nucleotides 2163-5747

encode for a POL polypeptide and nucleotides 5620-7590 encode for an ENV polypeptide. Alignment of these regions of SEQ ID NO: 3 with the GALV genome shows only 66, 66 and 60% identity for the GAG, POL and ENV polypeptides, respectively (see Attachments B, C and D).

In contrast to claim 44 part (c), Eiden et al. does not teach a nucleotide sequence which has 75% identity with a nucleotide sequence set forth in SEQ ID NOs: 1, 2, 3 or 9. As discussed above, the GALV genome only has 64% identitiy with SEQ ID NO: 3 of the instant application. Eiden et al. also does not teach a nucleotide sequence which has 75% identity with a portion of SEQ ID NOs: 1, 2, 3 or 9 which encode for at least one porcine retrovirus polypeptide. As discussed above, nucleotides 588-2162 of SEQ ID NO: 3 of the instant Application encode for GAG polypeptide, nucleotides 2163-5747 encode for a POL polypeptide and nucleotides 5620-7590 encode for an ENV polypeptide. The GALV genome only has 66, 66 and 60% identity with these regions, respectively.

In contrast to claim 44 part (d), Eiden et al. does not teach a nucleotide sequence which is complementary to a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9. Eiden et al. also does not teach a nucleotide sequence which is complementary to a portion of SEQ ID NOs: 1, 2, 3 or 9 which encodes for at least one porcine retrovirus polypeptide. Further, Eiden et al. does not teach a nucleotide sequence which is complementary to a nucleotide sequence which is 75% identical to SEQ ID NOs: 1, 2, 3 or 9, or a portion thereof which encodes for at least one porcine retrovirus polypeptide.

Therefore, there can be no anticipation. In view thereof, reconsideration and withdrawal of the rejections are respectfully requested.

The Action also notes that the sequence disclosed by Eiden et al. teaches some of the limitations of the primers and probes encompassed by the instant invention. Applicant's wish to point to out Eiden et al. does not anticipate the probes and primers as currently claimed.

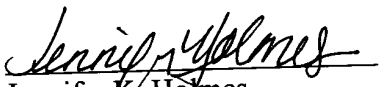
CONCLUSION

For the reasons presented, Applicants respectfully request that the pending rejections be reconsidered and withdrawn. Applicants believe that the claims are now in condition for allowance and early notification to this effect is earnestly solicited.

If there are any fees in connection with the filing of this Response, please charge the fees to our **Deposit Account No. 06-1448.** If a fee is required for an extension of time under 37 C.F.R. §1.136, such an extension is requested and the fee should also be charged to our Deposit Account.

Respectfully submitted,
Foley, Hoag & Eliot LLP

Dated: April 30, 2001



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Marked-up version of the amendments to the Specification showing changes made:

On page 1, below the title, please insert the following new line:

Background of the Invention

On page 2, after line 10, please insert the following new paragraphs:

Brief Description of the Drawings

Figure 1 shows a nucleic acid sequence from a cDNA isolated from PoEV having the sequence of SEQ ID NO: 1.

Figure 2 shows a nucleic acid sequence from a cDNA isolated from PoEV having the sequence of SEQ ID NO: 2.

Figure 3 shows a nucleic acid sequence from a cDNA isolated from PoEV having the sequence of SEQ ID NO: 3. Also depicted are the amino acid sequences produced by the 3 ORFs encoded by SEQ ID NO: 3 including (i) the *gag* gene encoding for a polypeptide having the amino acid sequence of SEQ ID NO: 4 (corresponding to nucleotides 588-2162 of SEQ ID NO: 3); (ii) the *pol* gene encoding for a polypeptide having the amino sequence of SEQ ID NO: 5 (corresponding to nucleotides 2163-5747 of SEQ ID NO: 3); and (iii) the *env* gene encoding for a polypeptide having the amino sequence of SEQ ID NO: 6 (corresponding to nucleotides 5620-7590 of SEQ ID NO: 3).

Figure 4 (top) shows a list of changes to the PoEV nucleic acid sequence (as compared to the sequence depicted in Figure 3) which were found in PoEV DNA isolated from PoEV infected Raji cells. The bottom half shows a list of changes to the ENV polypeptide (as compared to the sequence depicted in Figure 3) resulting from the nucleotide changes shown in the top half of the figure. SEQ ID NO: 9 is a nucleic acid sequence corresponding to nucleotides 5260-8210 of SEQ ID NO: 3 and containing the specified modifications. SEQ ID NO: 10 is an amino acid sequence corresponding to the ENV polypeptide of SEQ ID NO: 6 and containing the specified modifications.

Figure 5 shows a phylogenetic tree for the POL polypeptide.

Figure 6 the nucleotide sequence for a portion of the PoEV genome corresponding to the U3 region and depicting the multiple potential transcription sites located therein (SEQ ID NO: 17).

Detailed Description of the Invention

On page 23, please replace the second full paragraph with the following paragraph:

The changes at base nos. 5902 and 7700 do not effect the corresponding amino acid sequence. However, the changes at positions 2121 and 2157 alter the amino acid sequence at the end of GAG and the beginning of POL. For GAG the final amino acid "S" have now been replaced by "VLALEEDKD" (SEQ ID NO: 15). The total product size is now 524 amino acids. For POL, the first five amino acids "RLGET" (SEQ ID NO: 16) have been deleted and replaced by "GRR". The total product size is now 1194 amino acids.

On page 28, please replace the paragraph beginning at the top of the page with the following:

Oligonucleotides were selected from the PoEV genome.

The upstream primer was 5'-GGA AGT GGA CTT CAC TGA G-3' (SEQ ID NO: 7).

The downstream primer was 5'-CTT TCC ACC CCG AAT CGG-3' (SEQ ID NO: 8).

On page 29, please replace the second paragraph with the following:

Two further [digonucleotides] oligonucleotides were designed against the 3' end of the *pol* gene and [s'] 5' end of the *gag* gene respectively.

The 3' *pol* [oligionucleotide] oligonucleotide was 5'-GAT GGC TCT CCT GCC CTT TG-3' (SEQ ID NO: 11).

The 5' *gag* [oligionucleotide] oligonucleotide was 5'-CGA TGG AGG CGA AGC TTA AGG-3' (SEQ ID NO: 12).

On page 32, please replace the paragraph following the heading PCR with the following:

Oligonucleotides were selected from the PoEV genome.

The upstream primer was 5'-GAT GGC TCT CCT GCC CTT TG-3' (SEQ ID NO: 13)

5' base position: 5240.

The downstream primer was 5'-CCA CAG TCG TAC ACC ACG-3' (SEQ ID NO: 14)

5' base position: 8144.

Expected product size: 2904 bp.

On page 34, please replace the text following "Phylogenetic analysis" with the following:

Phylogenetic analysis was performed using the PHYLIP package. Sequence distances were calculated using the PROTDIST program (Dayhoff matrix) and a neighbour-joining unrooted phylogenetic tree reconstructed using the NEIGHBOUR program.

Bootstrapping was performed using 200 replicates of the *pol* alignment, created using the SEQBOOT program and a consensus tree was obtained using the CONSENSE program [(see Figure J)] (see Figure 5). The bootstrap percentages are indicated at the branch fork, with missing values equal to 100%. The data indicate that PoEV is closely related to but distinct from the type-C oncovirus typified by gibbon, murine and feline leukaemia viruses.

A phylogenetic tree was constructed from the *pol* alignment using the maximum likliehood algorithm (Dayhoff matrix). This tree differed from the *pol* NJ tree only in the placement of the BaEV lineage in relation to other mammalian type C viruses and corresponded to a low bootstrap for the BaEV fork observed in the NJ tree.

Marked-up version of the amendments to the claims:

Please cancel claims 1-43 and replace them with new claims 44-66 as set forth below:

44. (New) An isolated polynucleotide fragment comprising:

(a) a nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9;

(b) a portion of a nucleotide sequence set forth in (a) which encodes for at least one porcine retrovirus polypeptide;

(c) a nucleotide sequence which has at least 75% identity to a sequence set forth in (a) or (b); or

(d) a nucleotide sequence which is complementary to a nucleotide sequence set forth in (a), (b) or (c).

45. (New) An isolated polynucleotide fragment of claim 44, wherein the polynucleotide fragment encodes for a polymerase polypeptide (POL).

46. (New) An isolated polynucleotide fragment of claim 44, wherein the polynucleotide fragment encodes for a virion core polypeptide (GAG).

47. (New) An isolated polynucleotide fragment of claim 44, wherein the polynucleotide fragment encodes for an envelope polypeptide (ENV).

48. (New) An isolated polynucleotide fragment of claim 44, wherein the polynucleotide fragment encodes for a virion core polypeptide (GAG) and an envelope polypeptide (ENV).

49. (New) An isolated polynucleotide fragment encoding for a polypeptide comprising the amino acid sequence set forth in SEQ ID NO: 4, 5, 6 or 10.

50. (New) An isolated polynucleotide fragment comprising a nucleotide sequence which has at least 90% identity to a sequence set forth in SEQ ID NO: 1, 2, 3 or 9, or a nucleotide sequence which is complementary thereto.

51. (New) An isolated polynucleotide fragment of claim 50, which encodes for a virion core (GAG), a polymerase (POL) and an envelope (ENV) polypeptide.

52. (New) A recombinant nucleic acid molecule comprising a polynucleotide fragment according to claim 44.

53. (New) A recombinant nucleic acid molecule according to claim 52 wherein the recombinant nucleic acid molecule comprises regulatory control sequences operably linked to said polynucleotide fragment for controlling expression of said polynucleotide fragment.

54. (New) A vector comprising a polynucleotide fragment according to claim 44.

55. (New) A vector according to claim 54, which is a virus or a plasmid.

56. (New) A prokaryotic or eukaryotic host cell comprising a polynucleotide fragment according to claim 44.

57. (New) An oligonucleotide comprising at least 30 nucleotides which are fully complementary to a sequence set forth in claim 44.

58. (New) An oligonucleotide according to claim 57 which has the nucleotide sequence set forth in SEQ ID NO: 7, 8, 11, 12, 13 or 14.

59. (New) A PoEV detection kit comprising at least one oligonucleotide according to claim 57 or 58.

60. (New) A method for detecting PoEV in a nucleic acid containing sample comprising:

(a) contacting the sample with at least one oligonucleotide of claim 57 under hybridization conditions; and

(b) detecting hybridization of the oligonucleotide to the nucleic acid in the sample;

wherein detection of hybridization indicates that the sample contains PoEV.

61. (New) The method of claim 59, wherein the oligonucleotide contains a label.

62. (New) The method of claim 60, wherein the label is a radioactive, chemiluminescent or fluorescent label.

63. (New) A pair of oligonucleotide primers for use in PCR amplification wherein each primer comprises at least 10 nucleotides complementary to a sequence set forth in SEQ ID NO: 1, 2, 3 or 9, or a sequence complementary to a sequence set forth in SEQ ID NO: 1, 2, 3 or 9.

64. (New) A pair of oligonucleotide primers selected from the group consisting of SEQ ID NOs: 7 and 8, SEQ ID NOs: 11 and 12, and SEQ ID NOs: 13 and 14.

65. (New) A method for detecting PoEV in a nucleic acid containing sample comprising:

(a) contacting the sample with a pair of oligonucleotide primers as set forth in claim 63 or 64 under hybridization conditions;

(b) amplifying a nucleotide sequence between the two oligonucleotide primers; and

(c) detecting the presence of the amplified sequence;

wherein detection of the amplified sequence indicates that the sample contains PoEV.

66. (New) An antisense oligonucleotide complementary to a messenger RNA for a GAG, POL or ENV polypeptide encoded for by the nucleotide sequence set forth in SEQ ID NO: 1, 2, 3 or 9, wherein said antisense oligonucleotide suppresses expression of a PoEV GAG, POL or ENV polypeptide.